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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/853,257A

DATE: 10/30/2002  
TIME: 13:03:56

Input Set : A:\PUNIV.002A.TXT  
Output Set: N:\CRF4\10292002\I853257A.raw

ENTERED

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Input Set : A:\PUNIV.002A.TXT

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96 <210> SEQ ID NO: 2

97 <211> LENGTH: 491

98 <212> TYPE: PRT

99 <213> ORGANISM: *Vibrio harveyi*

101 4400s SEQUENCE: 2

162 Met Lys Pro Ser Leu Gln Leu Lys Leu Gln Gln Gln Leu Ala Met Thr

103 1 5 10 15

104 Pro Gln Leu Gln Gln Ala Ile Arg Leu Leu Gln Leu Ser Thr Leu Asp

10.5 20 25 30

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106 Leu Gln Gln Glu Ile Gln Glu Ala Leu Asp Ser Asn Pro Leu Leu Glu  
 107 35 40 45  
 108 Val Glu Glu Gly His Asp Glu Pro Gln Ala Asn Gly Glu Asp Lys Ser  
 109 50 55 60  
 110 Ala Ser Glu Ser Ala Asp Lys Ser Ala Asn Glu Ala Asn Asp Ala Ser  
 111 65 70 75 80  
 112 Glu Pro Asp Leu Pro Asp Ser Ser Asp Val Ile Glu Lys Ser Glu Ile  
 113 85 90 95  
 114 Ser Ser Glu Leu Glu Ile Asp Thr Thr Trp Asp Asp Val Tyr Ser Ala  
 115 100 105 110  
 116 Asn Thr Gly Ser Thr Gly Leu Ala Leu Asp Asp Asp Met Pro Val Tyr  
 117 115 120 125  
 118 Gln Gly Glu Thr Thr Glu Ser Leu His Asp Tyr Leu Met Trp Gln Leu  
 119 130 135 140  
 120 Asp Leu Thr Pro Phe Ser Glu Thr Asp Arg Thr Ile Ala Leu Ala Ile  
 121 145 150 155 160  
 122 Ile Asp Ala Val Asp Asp Tyr Gly Tyr Leu Thr Leu Ser Pro Glu Glu  
 123 165 170 175  
 124 Ile His Glu Ser Phe Asp Asn Glu Glu Val Glu Leu Asp Glu Val Glu  
 125 180 185 190  
 126 Ala Val Arg Lys Arg Ile Gln Gln Phe Asp Pro Leu Gly Val Ala Ser  
 127 195 200 205  
 128 Arg Asn Leu Gln Glu Cys Leu Leu Leu Gln Leu Ala Thr Phe Pro Glu  
 129 210 215 220  
 130 Asp Thr Pro Trp Leu Ala Glu Ala Lys Met Val Leu Ser Asp His Ile  
 131 225 230 235 240  
 132 Asp His Leu Gly Asn Arg Asp Tyr Lys Leu Val Ile Lys Glu Ala Lys  
 133 245 250 255  
 134 Leu Lys Glu Ala Asp Leu Arg Glu Val Leu Lys Leu Ile Gln Gln Leu  
 135 260 265 270  
 136 Asp Pro Arg Pro Gly Ser Arg Ile Thr Pro Asp Asp Thr Glu Tyr Val  
 137 275 280 285  
 138 Ile Pro Asp Val Ser Val Phe Lys Asp His Gly Lys Trp Thr Val Ser  
 139 290 295 300  
 140 Ile Asn Pro Asp Ser Ile Pro Lys Leu Lys Val Asn Gln Gln Tyr Ala  
 141 305 310 315 320  
 142 Gln Leu Gly Lys Gly Asn Ser Ala Asp Ser Gln Tyr Ile Arg Ser Asn  
 143 325 330 335  
 144 Leu Gln Glu Ala Lys Trp Leu Ile Lys Ser Leu Glu Ser Arg Asn Glu  
 145 340 345 350  
 146 Thr Leu Leu Lys Val Ala Arg Cys Ile Val Glu His Gln Gln Asp Phe  
 147 355 360 365  
 148 Phe Glu Tyr Gly Glu Glu Ala Met Lys Pro Met Val Leu Asn Asp Val  
 149 370 375 380  
 150 Ala Leu Asp Val Asp Met His Glu Ser Thr Ile Ser Arg Val Thr Thr  
 151 385 390 395 400  
 152 Gln Lys Phe Met His Thr Pro Arg Gly Ile Phe Glu Leu Lys Tyr Phe  
 153 405 410 415  
 154 Phe Ser Ser His Val Ser Thr Asp Asn Gly Gly Glu Cys Ser Ser Thr

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155 420 425 430  
156 Ala Ile Arg Ala Leu Ile Lys Lys Leu Val Ala Ala Glu Asn Thr Ala  
157 435 440 445  
158 Lys Pro Leu Ser Asp Ser Lys Ile Ala Ala Leu Leu Ala Asp Gln Gly  
159 450 455 460  
160 Ile Gln Val Ala Arg Arg Thr Ile Ala Lys Tyr Arg Glu Ser Leu Gly  
161 465 470 475 480  
162 Ile Ala Pro Ser Ser Gln Arg Lys Arg Leu Leu  
163 485 490  
166 <210> SEQ ID NO: 3  
167 <211> LENGTH: 176  
168 <212> TYPE: DNA  
169 <213> ORGANISM: Vibrio harveyi  
170 <400> SEQUENCE: 3  
171 atgaaacctt cattacaact caagcttagt caacagttag ccatgacgcc acagctgcag 60  
172 caagcgattt gtttgttgca attgtcgacg ctcgatcttc aacaagaat ccaagaagcg 120  
173 ttggqactcca acccgctact ggaagttgaa qaaggccacg atgagcctca agcaaatgg 180  
174 gaaqacaat cagcgtctga atctgctgat aaaagtgcga acgaagctaa cgatgcctca 240  
175 gaaaccgcacc ttccagatag ctcagacgtg attgaaaaat ctgaaatcatcg ctctgagcta 300  
176 gaaattgata ccacttggga tgacgtatat agcgc当地 a cgggcagcac aggcctagcg 360  
177 ctggatgatg acatgcccgt ctaccaaggt gagaccactg aatctttgca tgattacctt 420  
178 atgttgcagt tagacttaac gcctttca gaaaccgacc gcaccatcgc cctcgc 476  
181 <210> SEQ ID NO: 4  
182 <211> LENGTH: 6  
183 <212> TYPE: PRT  
184 <213> ORGANISM: Artificial Sequence  
186 <220> FEATURE:  
187 <223> OTHER INFORMATION: portion of consensus sequence of sigma-54 domains  
W--> 189 <221> NAME/KEY: VARIANT  
190 <222> LOCATION: (1)...(6)  
191 <223> OTHER INFORMATION: Xaa = Trp or Phe  
W--> 193 <400> 4  
W--> 194 Xaa Phe Pro Gly Asn Val  
195 1 5  
198 <210> SEQ ID NO: 5  
199 <211> LENGTH: 6  
200 <212> TYPE: PRT  
201 <213> ORGANISM: Artificial Sequence  
203 <220> FEATURE:  
204 <223> OTHER INFORMATION: portion of consensus sequence of sigma-54 domains  
W--> 206 <221> NAME/KEY: VARIANT  
207 <222> LOCATION: (1)...(6)  
208 <223> OTHER INFORMATION: Xaa = Val, Ala, Asp, Glu, Gly  
W--> 210 <400> 5  
W--> 211 Glu Leu Phe Gly His Xaa  
212 1 5  
215 <210> SEQ ID NO: 6  
216 <211> LENGTH: 20  
217 <212> TYPE: DNA

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218 <213> ORGANISM: Artificial Sequence  
 220 <220> FEATURE:  
 221 <223> OTHER INFORMATION: upstream primer to amplify rpoN gene  
 223 <400> SEQUENCE: 6  
 224 tquycaacart tagcstatgac 20  
 226 <210> SEQ ID NO: 7  
 227 <211> LENGTH: 21  
 228 <212> TYPE: DNA  
 229 <213> ORGANISM: Artificial Sequence  
 230 <220> FEATURE:  
 232 <223> OTHER INFORMATION: downstream primer to amplify rpoN gene  
 234 <400> SEQUENCE: 7  
 235 catsgcytcy tewccatact c 21  
 237 <210> SEQ ID NO: 8  
 238 <211> LENGTH: 25  
 239 <212> TYPE: DNA  
 240 <213> ORGANISM: Artificial Sequence  
 242 <220> FEATURE:  
 243 <223> OTHER INFORMATION: upstream primer used to amplify rpoN gene  
 245 <400> SEQUENCE: 8  
 246 tquaacggtaq aattctgagc attac 25  
 248 <210> SEQ ID NO: 9  
 249 <211> LENGTH: 38  
 250 <212> TYPE: DNA  
 251 <213> ORGANISM: Artificial Sequence  
 253 <220> FEATURE:  
 254 <223> OTHER INFORMATION: downstream primer used to amplify rpoN gene  
 256 <400> SEQUENCE: 9  
 257 ccttttgaat tcgtgcctaa agtaggcg 28  
 259 <210> SEQ ID NO: 10  
 260 <211> LENGTH: 222  
 261 <212> TYPE: PRT  
 262 <213> ORGANISM: V. harveyi  
 264 <400> SEQUENCE: 10  
 265 Ile Gly Ser Ser Gln Thr Met Gln Gln Val Tyr Arg Thr Ile Asp Ser  
 266 1 5 10 15  
 267 Ala Ala Ser Ser Lys Ala Ser Ile Phe Ile Thr Gly Glu Ser Gly Thr  
 268 20 25 30  
 269 Gly Lys Glu Val Cys Ala Glu Ala Ile His Ala Ala Ser Lys Arg Gly  
 270 35 40 45  
 271 Asp Lys Pro Phe Ile Ala Ile Asn Cys Ala Ala Ile Pro Lys Asp Leu  
 272 50 55 60  
 273 Ile Glu Ser Glu Leu Phe Gly His Val Lys Gly Ala Phe Thr Gly Ala  
 274 65 70 75 80  
 275 Ala Asn Asp Arg Gln Gly Ala Ala Glu Leu Ala Asp Gly Gly Thr Leu  
 276 85 90 95  
 277 Phe Leu Asp Glu Leu Cys Glu Met Asp Leu Asp Leu Gln Thr Lys Leu  
 278 100 105 110  
 279 Leu Arg Phe Ile Gln Thr Gly Ile Phe Gln Lys Val Gly Ser Ser Lys

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/30/2002  
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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq# : 4; Xaa Pos. 1  
Seq# : 5; Xaa Pos. 6